We claim:

1. A modified cytochrome P450 monooxygenase which, in comparison with the wild-type enzyme, shows an altered substrate profile in the terminal and/or subterminal enzymatic hydroxylation of aliphatic carboxylic acids, owing to site-specific mutagenesis of its substrate binding region.

2. A monooxygenase as claimed in claim 1, which is derived from cytochrome P450 monooxygenases of bacterial origin.

3. A monooxygenase as claimed in claim 2, which is derived from Bacillus megaterium cytochrome P450 monooxygenase BM-3 with an amino acid sequence in accordance with SEQ ID NO: 2, which has at least one functional mutation in one of the following amino acid sequence regions: 24-28, 45-51, 70-72, 73-82, 86-88, 172-224 und 352-356, with the proviso that, if the enzyme carries the mutation F87A, more than one of these regions is mutated.

4. A monooxygenase as claimed in claim 3, which comprises at least one functional mutation in the amino acid sequence regions 86-88 and 172-224.

5. A monooxygenase as claimed in claim 4, which comprises at least one of the following amino acid substitution patterns:

a) F87V;
b) F87A L188K;
c) F87V L188K;
d) F87A L188K A74G;
e) F87V L188K A74G;
f) F87A L188K A74G R47F;
g) F87V L188K A74G R47F;
h) F87A L188K A74G R47F V26T; or
i) F87V L188K A74G R47F V26T;

and functional equivalents thereof.

6. A monooxygenase as claimed in claim 3, which comprises a single amino acid substitution from amongst the following:

a) V26T,
b) R47F,
c) S72G,
d) A74G,

e) F87V,

f) L188z, where Z is an amino acid selected from amongst K, R, W, Q, N, G, A and S, and

g) M354T;

and functional equivalents thereof.

7. A nucleic acid sequence encoding a monooxygenase as claimed in any of the preceding claims and the complementary nucleic acid sequence thereof.

8. An expression construct comprising, under the genetic control of regulatory nucleic acid sequences, an encoding sequence which encompasses a nucleic acid sequence as claimed in claim 7.

9. A vector which encompasses at least one expression construct as claimed in claim 8.

10. A recombinant microorganism which has been transformed with at least one vector as claimed in claim 9.

11. A microorganism as claimed in claim 10, selected from amongst bacteria of the genus Escherichia.

12. A process for the enzymatic production of terminally or subterminally hydroxylated aliphatic carboxylic acids, which comprises

a1) culturing a recombinant microorganism as claimed in claim 10 or 11 according to the invention in the presence of a culture medium which contains at least one hydroxylatable carboxylic acid or at least one hydroxylatable carboxylic acid derivative; or

a2) incubating a reaction medium containing at least one hydroxylatable carboxylic acid or at least one hydroxylatable carboxylic acid derivative with an enzyme as claimed in any of claims 1 to 6, and

b) isolating the resulting hydroxylated product from the medium.

13. A method as claimed in claim 12, wherein the hydroxylatable carboxylic acid is a C_8-C_{30} monocarboxylic acid or a derivative thereof.

14. A method as claimed in claim 13, wherein the hydroxylatable carboxylic acid is a C_8-C_{12}-monocarboxylic acid or a derivative thereof and the monooxygenase used is a mutant as claimed in claim 5.

15. A method as claimed in claim 13, wherein the hydroxylatable carboxylic acid is a C_{12}-C_{30}-monocarboxylic acid or a derivative thereof and the monooxygenase employed is a mutant selected from amongst the single mutants F87A, F87V, V26T, S72G, A74G and M354T, and the multiple mutants
F87A L188K A74G R47F;
F87V L188K A74G R47F;
F87A L188K A74G R47F V26T; or
F87V L188K A74G R47F V26T.

16. A method as claimed in any of claims 12 to 15, wherein the reaction is carried out in the presence of an electron donor or a reduction equivalent.

17. A method as claimed in claim 16, wherein the electron donor or the reduction equivalent is selected from amongst NADH, NADPH and Zn/Co(III) sepulchrate.